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P#9

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1645

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/698,213ADATE: 05/21/2001
TIME: 10:43:56Input Set : A:\SeqList.txt
Output Set: N:\CRF3\05212001\I698213A.raw

ENTERED

2 <110> APPLICANT: McIninch, James
 4 <120> TITLE OF INVENTION: COMPUTATIONAL NUCLEIC ACID CODING AND FEATURE ANALYSIS
 6 <130> FILE REFERENCE: 04983.0220.00US00
 8 <140> CURRENT APPLICATION NUMBER: 09/698,213A
 10 <141> CURRENT FILING DATE: 2000-10-30
 12 <160> NUMBER OF SEQ ID NOS: 13
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2165
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Arabidopsis thaliana
 21 <220> FEATURE:
 22 <221> NAME/KEY: unsure
 23 <222> LOCATION: (1)...(2165)
 24 <223> OTHER INFORMATION: Unsure at all n locations
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Ecotype Landsberg, genomic DNA
 29 <400> SEQUENCE: 1

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32	cgtttttcc gagcattgta ggccgtcctc gcccacaccgg tggatgtgtt gggatgggac	120
34	aaaaggatgc ttatgttggaa gacgaggcgc aatcaaaaacg tggtatctt actctgaagt	180
36	acccaattga gcatggaaatt gttaataatt gggatgacat ggagaagatt tggcatcaca	240
38	ctttctacaa tgagcttcgt gttccccctg aagaacatcc ggttctctt accgaagctc	300
40	cctctaattcc gaaagctaac cgtgagaaga tgactcagat catgttttag acattcaata	360
42	ctcctgctat gtatgttgc attcaagctg ttctctcaact ctatgccagt ggcgtacta	420
44	ctggcagta cattactaca ttctttttat accgttttgt taaaataaaa ttcggtttgg	480
46	ttcgattcga gtttgccttc attatttttta ttgttgtgt taggtatgt tttgactcc	540
48	ggagatggtg tgagccacac ggtaccaatc tacgagggtt atgcacttcc acacgcaatc	600
50	ctgcgtcttgc atcttgcagg tcgtgaccta accggacc ttatggaaat cctgacagag	660
52	cgtggtaact ctttcaccc aactgtcgag cgtgagatgg tttagacat gaaggagaag	720
54	ctctcttaca ttgccttggaa ctttgcacaa gagctcgaga cttccaaac aagctcatcc	780
56	gttgagaaga gcttcgagct gccagacggt caagtgtatca ccattggggc agagcggttc	840
58	cgtgccctg aagttctgtt tcagccatcg atgatcgaa tggaaatcc gggattcat	900
60	gaaactactt acaactaat catggaaatgt gatgtggata tcaggaagga tctttatggaa	960
62	aacattgtgc ttgttgttgc caccacaatg ttgcgtggaa ttgtgtatag gatgataaa	1020
64	gagatcacag cgttggctcc aagcgtatg aacatcaaag ttgttgttgc accggaaagg	1080
66	aagtacatgt tctggatcggt tggctctatc ttggcttccc tcagttttt ccagcaggta	1140
68	aattacttac tatacttaat acataaaatgc tattatgtat ttgtatgtata aagtgttaca	1200
70	aaaatgtgtt ccaaatttgc agatgtggat tgcgaaagcg gagatgtatg aatctggacc	1260
72	gtcaatcgtc cacaggaatg gcttcgtatc aaaagtccacc aagtaaaaaca agagcggtaa	1320
74	aaatttgtat atcgtttttt caccctgaag ccagttgtatca taattactca caacttctt	1380
76	atttgtgttc ttttatttttgc gtcctcggtt gttcattttta atctctttt tgcaacaaag	1440
78	caactaaaaaa aaacagagca gtcattaaaca gaatgttattt attatataat tttatataat	1500
80	ttatgtatata cccattattt cattaaaaaca ttatcatat aaggatagga ttctatataat	1560
82	cgatataattt attttgttgc cactattcag cacatgttta tgccttatct tttatgtata	1620
84	tgtaacccaa gacaataat agatgtatca aattgttttc tttgaagcaa aaatttcaat	1680
86	cttaaaatttgc ttgttgcacaa aaaaaacttgc tagttgtaa attttctata	1740

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88	caattttggg	gatctcaaca	agaacatgaa	cttcaacttc	tagtcataatg	acgaccgttag	1800									
90	tctgcgcggc	tgtgaatctc	tttgctcgag	taaatgttta	caagtgggt	gtaaattgggt	1860									
92	actgattcaa	aagcttaag	aatctacac	atttcgtgaa	attatttgc	agacttgata	1920									
94	ttaaaaaatct	aggataaaaat	gactatccaa	agacaaatag	gactgtttca	catgttcccc	1980									
96	tgattcttgt	agctcataac	tcatcagcag	ttaactttc	tacctcatac	acgctcgcaa	2040									
W--> 98	tncgtttgga	attatcagct	ntaatttttc	taatttcttg	gaaattatta	gcagctcgat	2100									
100	caaattgggc	atggcttctt	cttctatctg	caactcatct	aaactttcca	tgaagaaaca	2160									
102	aagct						2165									
105	<210>	SEQ ID NO:	2													
106	<211>	LENGTH:	6													
107	<212>	TYPE:	PRT													
108	<213>	ORGANISM:	Unknown													
110	<220>	FEATURE:														
111	<223>	OTHER INFORMATION:	Describes a predicted protein sequence													
113	<400>	SEQUENCE:	2													
114	Arg	Phe	Arg	Ala	Leu											
115	1					5										
118	<210>	SEQ ID NO:	3													
119	<211>	LENGTH:	7													
120	<212>	TYPE:	PRT													
121	<213>	ORGANISM:	Unknown													
123	<220>	FEATURE:														
124	<223>	OTHER INFORMATION:	Describes a predicted protein sequence													
126	<400>	SEQUENCE:	3													
127	Ala	Val	Leu	Ala	Thr	Pro	Val									
128	1					5										
131	<210>	SEQ ID NO:	4													
132	<211>	LENGTH:	21													
133	<212>	TYPE:	PRT													
134	<213>	ORGANISM:	Unknown													
136	<220>	FEATURE:														
137	<223>	OTHER INFORMATION:	Describes a predicted protein sequence													
139	<400>	SEQUENCE:	4													
140	Trp	Leu	Gly	Trp	Asp	Lys	Arg	Met	Leu	Met	Leu	Glu	Thr	Arg	Leu	Asn
141	1							5		10				15		
143	Gln	Asn	Val	Val	Ser											
144						20										
147	<210>	SEQ ID NO:	5													
148	<211>	LENGTH:	35													
149	<212>	TYPE:	PRT													
150	<213>	ORGANISM:	Unknown													
152	<220>	FEATURE:														
153	<223>	OTHER INFORMATION:	Describes a predicted protein sequence													
155	<400>	SEQUENCE:	5													
156	Ser	Thr	Gln	Leu	Ser	Met	Glu	Leu	Leu	Ile	Ile	Gly	Met	Thr	Trp	Arg
157	1					5				10				15		
159	Arg	Phe	Gly	Ile	Thr	Leu	Ser	Thr	Met	Ser	Phe	Val	Leu	Pro	Leu	Lys
160									20		25			30		
162	Asn	Ile	Arg													

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163      35
166 <210> SEQ ID NO: 6
167 <211> LENGTH: 56
168 <212> TYPE: PRT
169 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Describes a predicted protein sequence
174 <400> SEQUENCE: 6
175 Leu Thr Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr
176 1           5          10          15
177 Gln Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile
178 20          25          30
179 Gln Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Gln Tyr
180 35          40          45
181 Ile Thr Thr Phe Phe Leu Tyr Arg
182 50          55
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 191
185 <212> TYPE: PRT
186 <213> ORGANISM: Unknown
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Describes a predicted protein sequence
189 <400> SEQUENCE: 7
190 Ser Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala
191 1           5          10          15
192 Ser Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala
193 20          25          30
194 Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr
195 35          40          45
196 Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys Glu Lys Leu Ser Tyr
197 50          55          60
198 Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr Ser Lys Thr Ser Ser
199 65          70          75          80
200 Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
201 85          90          95
202 Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met
203 100         105         110
204 Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
205 115         120         125
206 Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val
207 130         135         140
208 Leu Ser Gly Gly Thr Thr Met Phe Asp Gly Ile Gly Asp Arg Met Ser
209 145         150         155         160
210 Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val
211 165         170         175
212 Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile
213 180         185         190
214 <210> SEQ ID NO: 8
215 <211> LENGTH: 13

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236 <212> TYPE: PRT
237 <213> ORGANISM: Unknown
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Describes a predicted protein sequence
242 <400> SEQUENCE: 8
243 Val Pro Asn Leu Gln Met Trp Ile Ala Lys Ala Glu Tyr
244 1 5 10
247 <210> SEQ ID NO: 9
248 <211> LENGTH: 26
249 <212> TYPE: PRT
250 <213> ORGANISM: Unknown
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Describes a predicted protein sequence
255 <400> SEQUENCE: 9
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257 1 5 10 15
259 Pro Ser Lys Thr Arg Ala Val Lys Ile Leu
260 20 25
263 <210> SEQ ID NO: 10
264 <211> LENGTH: 56
265 <212> TYPE: PRT
266 <213> ORGANISM: Unknown
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Describes a predicted protein sequence
271 <400> SEQUENCE: 10
273 Asn Ser Ser Ala Val Asn Phe Ser Thr Ser Tyr Thr Leu Ala Ile Arg
274 1 5 10 15
276 Leu Glu Leu Ser Ala Leu Ile Phe Leu Ile Ser Leu Glu Ile Ile Ser
277 20 25 30
279 Ser Ser Ile Lys Trp Gly Met Ala Ser Ser Ser Ile Cys Asn Ser Ser
280 35 40 45
282 Lys Leu Ser Met Lys Lys Gln Ser
283 50 55
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 194
288 <212> TYPE: PRT
289 <213> ORGANISM: Unknown
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Describes a predicted protein sequence
294 <400> SEQUENCE: 11
295 Ser Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala
296 1 5 10 15
298 Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
299 20 25 30
301 Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr
302 35 40 45
304 Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys Glu Lys Leu Ser Tyr
305 50 55 60
307 Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr Ser Lys Thr Ser Ser

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308 65 70 75 80
 310 Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
 311 85 90 95
 313 Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met
 314 100 105 110
 316 Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
 317 115 120 125
 319 Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val
 320 130 135 140
 322 Leu Ser Gly Gly Thr Thr Met Phe Asp Gly Ile Gly Asp Arg Met Ser
 323 145 150 155 160
 325 Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val
 326 165 170 175
 328 Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu
 329 180 185 190
 331 Ala Ser
 334 <210> SEQ ID NO: 12
 335 <211> LENGTH: 9
 336 <212> TYPE: PRT
 337 <213> ORGANISM: Unknown
 339 <220> FEATURE:
 340 <223> OTHER INFORMATION: Describes a predicted protein sequence
 342 <400> SEQUENCE: 12
 343 Gln Met Trp Ile Ala Lys Ala Glu Tyr
 344 1 5
 347 <210> SEQ ID NO: 13
 348 <211> LENGTH: 296
 349 <212> TYPE: PRT
 350 <213> ORGANISM: Arabidopsis thaliana
 352 <220> FEATURE:
 353 <223> OTHER INFORMATION: Ecotype columbia, describes actin
 355 <400> SEQUENCE: 13
 357 Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val Ala
 358 1 5 10 15
 360 Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro Lys
 361 20 25 30
 363 Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr
 364 35 40 45
 366 Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Ala Ser Gly
 367 50 55 60
 369 Arg Thr Thr Gly Gly Ile Val Leu Asp Ser Gly Asp Gly Val Ser His
 370 65 70 75 80
 372 Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg
 373 85 90 95
 375 Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp His Leu Met Lys Ile Leu
 376 100 105 110
 378 Thr Glu Arg Gly Tyr Ser Phe Thr Thr Ala Glu Arg Glu Ile Val
 379 115 120 125
 381 Arg Asp Met Lys Glu Lys Leu Ser Tyr Ile Ala Leu Asp Phe Gln

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/698,213A

DATE: 05/21/2001

TIME: 10:43:57

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\05212001\I698213A.raw

L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1